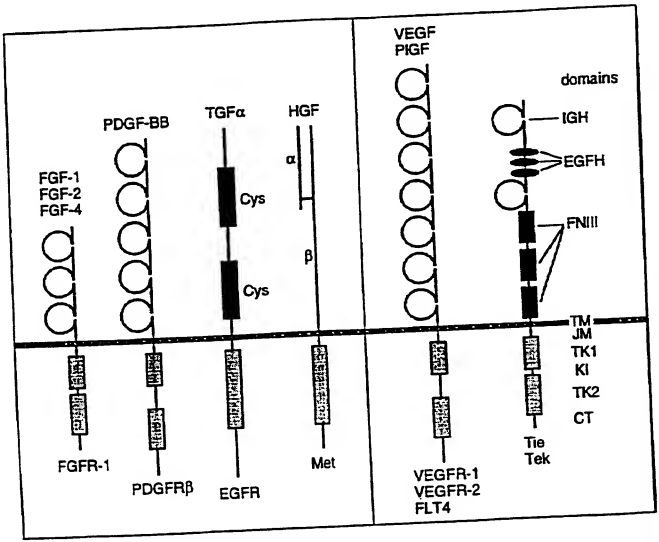
VEGF
PlGF
domains
PDGF-BB
TGFα
HGF
IGH
α
EGFH
FGF-1
FGF-2
FGF-4
Cys
FNIII
β
Cys
TM
JM
TK1
KI
TK2
CT
FGFR-1
PDGFRβ
EGFR
Met
Tie
Tek
VEGFR-1
VEGFR-2
FLT4

FIGURE 1

```
                1                                                    50
PDGF-A  .......... .......... .......... .......... .MRTLACLLL
PDGF-B  .......... .......... .......... .......... MNRCWA.LFL
P1GF-1  .......... .......... .......... .......... ..........
VEGF165 .......... .......... .......... .......... ..........
VEGF-B167 ......... .......... .......... .......... ..........
VEGF-C  MHLLGFFSVA CSLLAAALLP GPREAPAAAA AFESGLDLSD AEPDAGEATA

               51                                                   100
PDGF-A  LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE IDSVGSEDSL
PDGF-B  SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH GDP.GEEDGA
P1GF-1  .......... ......MPVM RLFPC..FLQ LLAGLAL... PAVPPQQW..
VEGF165 .......... .........M NFLLS..WVH WSLALLLYLH HAKWSQAA..
VEGF-B167 ......... .........M SPLLR..RLL LAALLQLAPA QAPVSQP...
VEGF-C  YASKDLEEQL RSVSSVDELM TVLYPEYWKM YKCQLRKGGW QHNREQANLN

              101                                                   150
PDGF-A  DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP AVCKTRTVIY
PDGF-B  ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI AECKTRTEVF
P1GF-1  .....ALSAG NGSSEVEVVP FQE.VWGR.. .......... SYCRALERLV
VEGF165 .....PMAEG GGQNHHEVVK FMD.VYQR.. .......... SYCHPIETLV
VEGF-B167 .........D APGHQRKVVS WID.VYTR.. .......... ATCQPREVVV
VEGF-C  SRTEETIKFA AAHYNTEILK SIDNEWRK.. .......... TQCMPREVCI

              151                                                   200
PDGF-A  EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS RVHHRSVKVA
PDGF-B  EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT QVQLRPVQVR
P1GF-1  DVVSEYPSEV ..EHMFSPSC VSLLRCTGCC GDENLHCVPV ETANVTMQLL
VEGF165 DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT EESNITMQIM
VEGF-B167 PLTVELMGTV ..AKQLVPSC VTVQRCGGCC PDDGLECVPT GQHQVRMQIL
VEGF-C  DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT STSYLSKTLF
```

FIGURE 2 A

```
                                                                  250
      201
PDGF-A    KVEYVRKKPK LKEVQVRLEE HLECACAT.. .......... TSLNPDYREE
PDGF-B    KIEIVRKKPI FKKATVTLED HLACKCETVA AARPVTRSPG GSQEQRAKTP
P1GF-1    KIRSG..DRP .SYVELTFSQ HVRCECRPLR EK........ ..........
VEGF165   RIKPH..QGQ .HIGEMSFLQ HNKCECRPKK DR........ ..........
VEGF-B167 MIRYP..SSQ ..LGEMSLEE HSQCECRPKK KD........ ..........
VEGF-C    EITVPLSQGP .KPVTISFAN HTSCRCMSKL DVYRQVHSII RRSLPATLPQ

                                                                  300
      251
PDGF-A    DTDVR..... .......... .......... .......... ..........
PDGF-B    QTRVTIRTVR VRRPPKGKHR KFKHTHDKTA LKETLGA... ..........
P1GF-1    .......... .......... .......... .MKPERCGDA VPRR......
VEGF165   .......... .......... .......... .ARQENPCGP CSERRKHLFV
VEGF-B167 .......... .......... .........S AVKPDSPRPL CPRCTQHHQR
VEGF-C    CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG FHDICGPNKE

                                                                  350
      301
PDGF-A    .......... .......... .......... .......... ..........
PDGF-B    .......... .......... .......... .......... ..........
P1GF-1    .......... .......... .......... .......... ..........
VEGF165   QDPQTCKCSC KNTDS.RCKA RQLELNERTC RCDKPRR... ..........
VEGF-B167 PDPRTCRCRC RRRSFLRCQG RGLELNPDTC RCRKLRR... ..........
VEGF-C    LDEETCQCVC RAGLRPASCG PHKELDRNSC QCVCKNKLFP SQCGANREFD
```

FIGURE 2 B

```
          351                                                       400
PDGF-A    .......... .......... .......... .......... ..........
PDGF-B    .......... .......... .......... .......... ..........
P1GF-1    .......... .......... .......... .......... ..........
VEGF165   .......... .......... .......... .......... ..........
VEGF-B167 .......... .......... .......... .......... ..........
VEGF-C    ENTCQCVCKR TCPRNQPLNP GKCACECTES PQKCLLKGKK FHHQTCSCYR

          401                                       434
PDGF-A    .......... .......... .......... ....
PDGF-B    .......... .......... .......... ....
P1GF-1    .......... .......... .......... ....
VEGF165   .......... .......... .......... ....
VEGF-B167 .......... .......... .......... ....
VEGF-C    RPCTNRQKAC EPGFSYSEEV CRCVPSYWKR PQMS
```

FIGURE 2 C

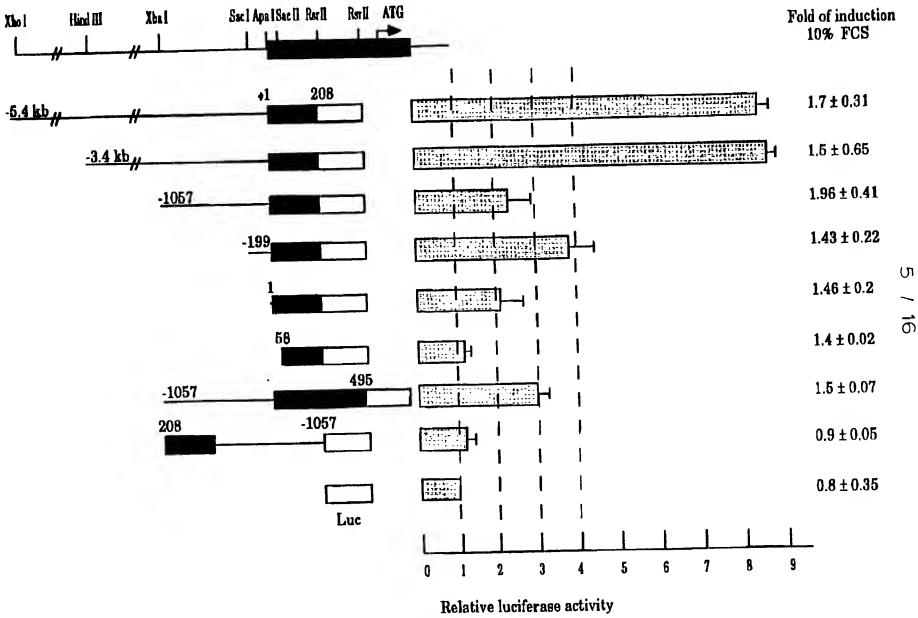

FIGURE 3

FIGURE 4B

FIGURE 4A

VEGF-C alignment

```
                                                             50
     1
Hum  HMLLGFFSVA CSLLAAALLP GPREAPAAAA AFESGLDLSD AEPDAGEATA
Mou  MHLLCFLSLA CSLLAAALIP SPREAPATVA AFESGLGFSE AEPDGGEVKA
Qua  MHLLEMLSLG CCLAAGAVLL GPRQPPVA.A AYESGHGYYE EEPGAGEPKA

                                                            100
     51
Hum  YASKDLEEQL RSVSSVDELM TVLYPEYWKM YKCQLRKGGW QHNREQANLN
Mou  FEGKDLEEQL RSVSSVDELM SVLYPDYWKM YKCQLRKGGW Q....QPTLN
Qua  HASKDLEEQL RSVSSVDELM TVLYPEYWKM FKCQLRKGGW QHNREHSSSD

                                                            150
     101
Hum  SRTEETIKFA AAHYNTEILK SIDNEWRKTQ CMPREVCIDV GKEFGVATNT
Mou  TRTGDSVKFA AAHYNTEILK SIDNEWRKTQ CMPREVCIDV GKEFGAATNT
Qua  TRSDDSLKFA AAHYNAEILK SIDTEWRKTQ GMPREVCVDL GKEFGATTNT

                                                            200
     151
Hum  FFKPPCVSVY RCGGCCNSEG LQCMNTSTSY LSKTLFEITV PLSQGPKPVT
Mou  FFKPPCVSVY RCGGCCNSEG LQCMNTSTGY LSKTLFEITV PLSQGPKPVT
Qua  FFKPPCVSIY RCGGCCNSEG LQCMNISTNY ISKTLFEITV PLSHGPKPVT

                                                            250
     201
Hum  ISFANHTSCR CMSKLDVYRQ VHSIIRRSLP ATLPQCQAAN KTCPTNYMWN
Mou  ISFANHTSCR CMSKLDVYRQ VHSIIRRSLP ATLPQCQAAN KTCPTNYVWN
Qua  VSFANHTSCR CMSKLDVYRQ VHSIIRRSLP ATQTQCHVAN KTCPKNHVWN

                                                            300
     251
Hum  NHICRCLAQE DFMFSSDAGD DSTDGFHDIC GPNKELDEET CQCVCRAGLR
Mou  NYMCRCLAQQ DFIFYSNVED DSTNGFHDVC GPNKELDEDT CQCVCKGGLR
Qua  NQICRCLAQH DFGFSSHLGD SDTSEGFHIC GPNKELDEET CQCVCKGGVR

                                                            350
     301
Hum  PASCGPHKEL DRNSCQCVCK NKLFPSQCGA NREFDENTCQ CVCKRTCPRN
Mou  PSSCGPHKEL DRDSCQCVCK NKLFPNSCGA NREFDENTCQ CVCKRTCPRN
Qua  PISCGPHKEL DRASCQCMCK NKLLPSSCGP NKEFDEEKCQ CVCKKTCPKH

                                                            400
     351
Hum  QPLNPGKCAC ECTESPQKCL LKGKKFHHQT CSCYRRPCTN RQKACEPGFS
Mou  QPLNPGKCAC ECTENTQKCF LKGKKFHHQT CSCYRRPCAN RLKHCDPGLS
Qua  HPLNPAKCIC ECTESPNKCF LKGKRFHHQT CSCYRPPCTV RTKRCDAGFL

     401                   420
Hum  YSEEVCRCVP SYWKRPQMS*
Mou  FSEEVCRCVP SYWKRPHLN.
Qua  LAEEVCRCVR TSWKRPLMN*
```

FIGURE 5

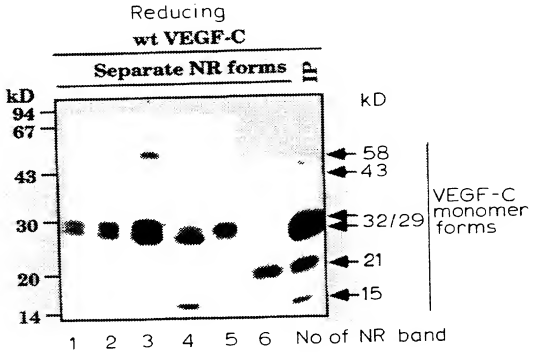

FIGURE 6A

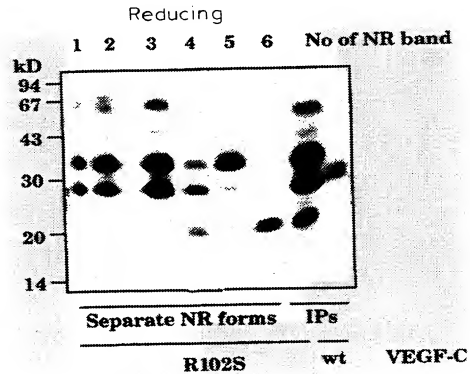

FIGURE 6C

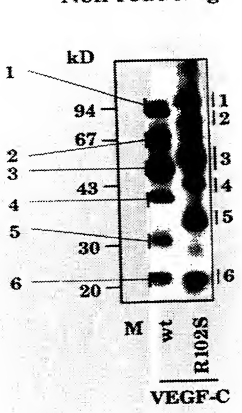

FIGURE 6B

MEDIA

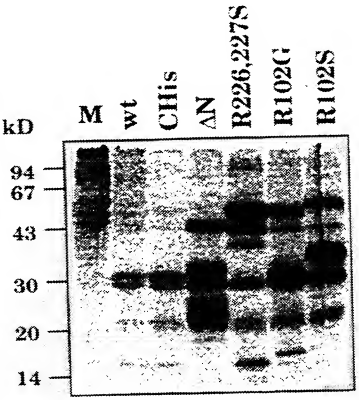

FIGURE 7A

LYSATES

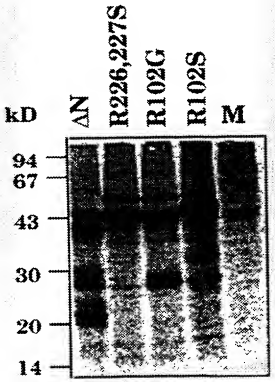

FIGURE 7B

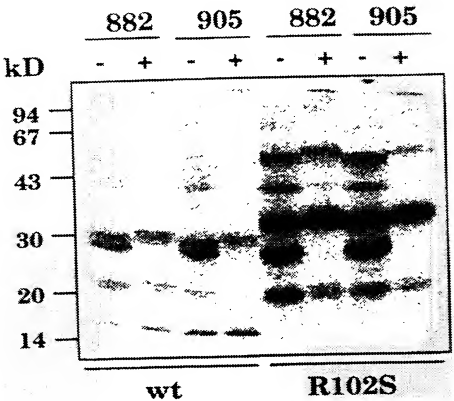

FIGURE 8A

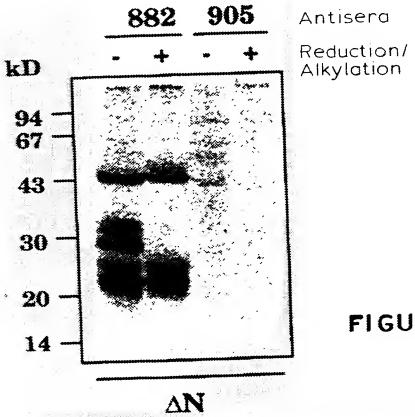

FIGURE 8B

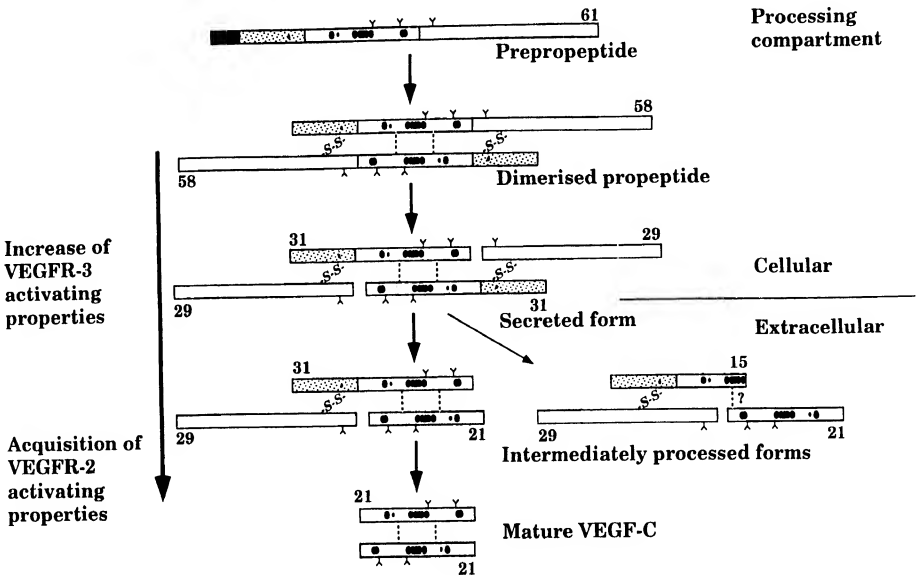

FIGURE 9

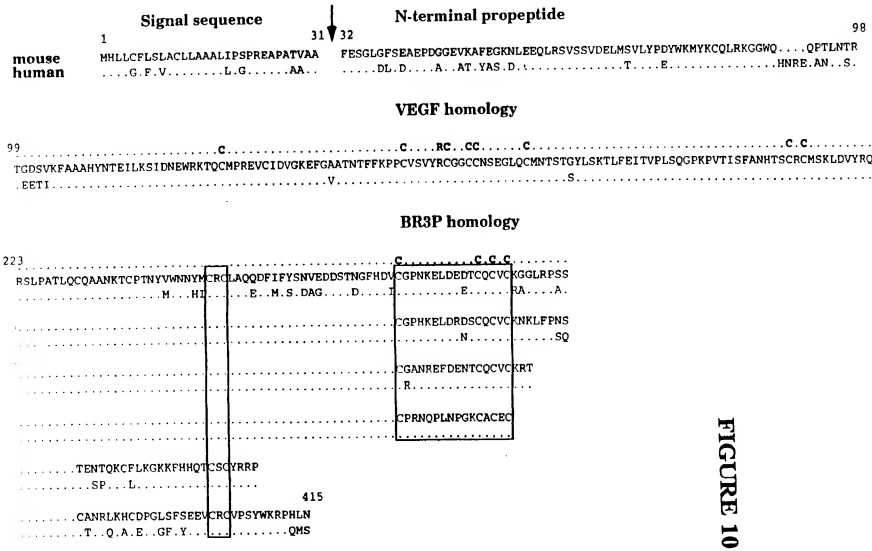

FIGURE 10

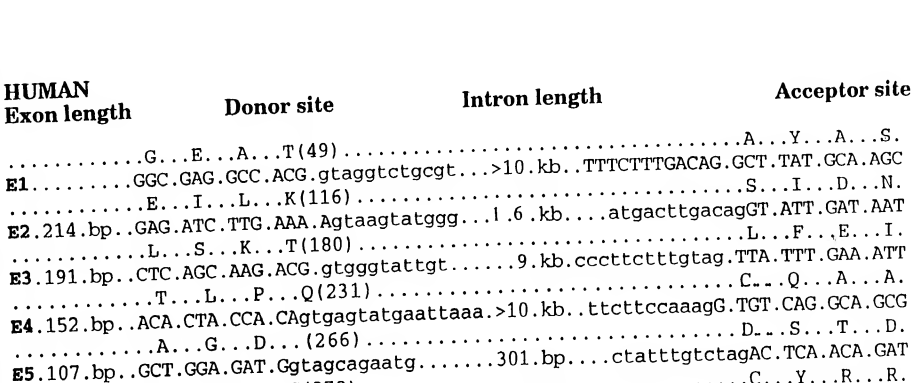

FIGURE 11A

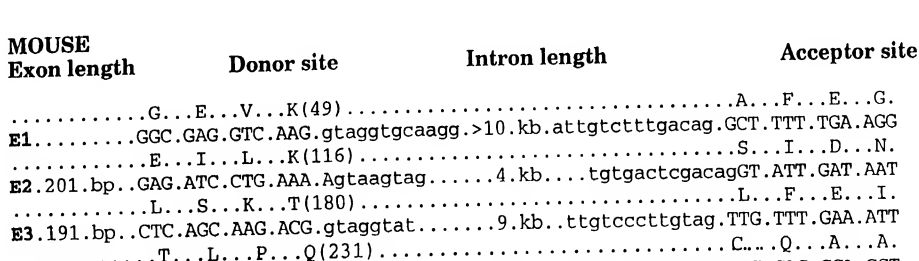

FIGURE 11B

Schematic structure of the human VEGF-C gene

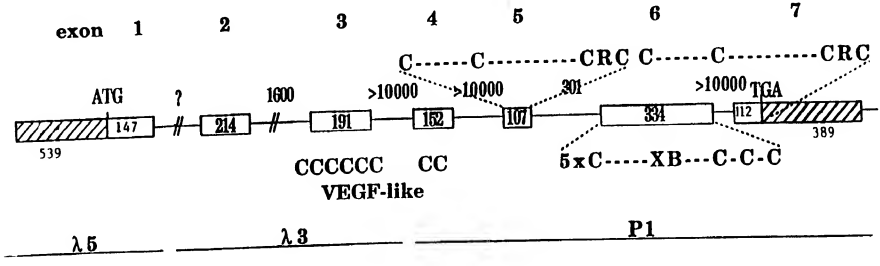

FIGURE 12